



# STIC Search Report

## Biotech-Chem Library

File Copy  
09/671,687  
updated

STIC Database Tracking Number: 150771

TO: David Lamberston  
Location: rem/2b79/2c70  
Art Unit: 1636  
Tuesday, April 19, 2005

Case Serial Number: 09/671687

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Lamberston,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC-Biotech/ChemLib

150771

mg

From: Lambertson, David  
Sent: Friday, April 15, 2005 10:25 AM  
To: STIC-Biotech/ChemLib  
Cc: Lambertson, David  
Subject: Search Request

(STIC)

APR 15 2005

RECEIVED

## Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	02B79 Remsen
Mailbox room#:	02C70 Remsen
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/671687

Please Search:

Protein and Nucleic Acid databases for:

SEQ ID No: 3

Including:

1. Default Search.
2. Oligomer Search.
3. Interference Search.

Thanks,  
Dave.

4/15/05  
1-AA-028  
1-AA-7NN  
038

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:14:54 ; Search time 73 Seconds

(without alignment)

5027.885 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQEKVTSFWBERI.....RLLCDAYMCMVQSPMSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004as.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4983	99.0	953	7	ADC24816 Human bre
2	4983	99.0	953	8	Adq95918 T cell ac
3	4980	99.0	960	8	Adr99244 DKFZp586D
4	4980	98.9	953	8	Adq95916 T cell ac
5	4971.5	98.8	956	6	Abb82783 Human CYL
6	4971.5	98.8	956	8	Adr14489 Human NF-
7	4968.5	98.7	956	8	Adq95920 T cell ac
8	3876.5	77.0	739	4	Aau23747 Novel hum
9	3862	76.7	731	3	Aay91954 Human cyt
10	3855	76.6	731	4	Aab95828 Human pro
11	3636	72.2	685	4	Aam39254 Human pol
12	3563	70.8	698	4	Aam41040 Human pol
13	2755	54.7	558	4	Aau23211 Novel hum
14	2343	46.5	476	4	Abb95719 Human pro
15	1275	25.3	261	5	Abb89233 Human pol
16	1173	23.3	238	5	Abb89234 Human pol
17	856	17.0	517	4	Abb61669 Drosophil
18	597	11.9	113	4	Aam14965 Peptide #
19	597	11.9	113	4	Abb33941 Peptide #
20	597	11.9	113	4	Aam27399 Peptide #
21	597	11.9	113	4	Abb28754 Peptide #
22	597	11.9	113	4	Abb19377 Peptide #
23	597	11.9	113	4	Aam67104 Human bon
24	597	11.9	113	4	Aam54704 Human bra
25	597	11.9	113	4	Aam02691 Peptide #

26	597	11.9	113	5	ABG36764 Human pep
27	568	11.3	106	8	Adk71947 Human ori
28	548	10.8	101	8	Adk71945 Human ori
29	514	10.2	96	8	Adk71949 Human ori
30	492	9.8	104	8	Adk71962 Human ori
31	491	9.8	91	8	Adk71943 Human ori
32	151	3.0	1392	2	Aay06999 Restin pr
33	151	3.0	1427	8	Adp56353 Human PRO
34	149	3.0	1427	2	Aar10534 Human 160
35	146	2.9	354	7	Abm85235 Human pro
36	143	2.8	547	5	Aau74342 Human cyt
37	143	2.8	547	5	ABB97353 Novel hum
38	143	2.8	547	7	ADM04066 Human pro
39	139.5	2.8	1921	4	ABB62962 Drosophil
40	136	2.7	708	8	ADN99865 Novel hum
41	135.5	2.7	306	3	AAB42642 Human ORF
42	135.5	2.7	306	7	ADB64836 Human PRO
43	135.5	2.7	721	4	Aau87339 Novel cen
44	135.5	2.7	721	8	ADIS4654 Novel hum
45	135.5	2.7	2273	6	ABU38191 Protein e

## ALIGNMENTS

### RESULT 1

ADC24816

ID ADC24816 standard; protein; 953 AA.

XX AC ADC24816;

XX AC ADC24816;

DT 18-DEC-2003 (first entry)

XX Human breast specific polypeptide (BSP) DEX0238\_137, SEQ ID NO:137.

DE Human breast specific polypeptide (BSP) DEX0238\_137, SEQ ID NO:137.

KW Human; breast specific polypeptide; BSP; breast specific nucleic acid;

KW BSNAs; breast cancer; metastasis; non-cancerous disease; breast tissue;

KW identification; monitoring; diagnosis;

KW engineered breast tissue production; transgenic animal; drug screening;

KW cytostatic; gene therapy; vaccine; chromosome 16p13.3.

XX Homo sapiens.

XX WO2003020900-A2.

XX 13-MAR-2003.

XX 29-AUG-2002; 2002WO-US027777.

XX 31-AUG-2001; 2001US-0316306P.

XX (DIAD-) DIADEXUS INC.

XX Sun Y, Liu C, Salceda S;

XX WPI; 2003-290182/28.

XX N-PSDB; ADC24898.

XX New breast specific polypeptide useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast.

XX Disclosure; SEQ ID NO 137; 264pp; English.

XX The invention relates to breast specific polypeptides (BSPs) and nucleic acids (breast specific nucleic acids; BSNAs) encoding them. The invention also relates to vectors and host cells comprising a BSNAs sequence.

XX Antibodies against BSPs; the recombinant production of BSPs; methods of detection of BSNAs or BSPs in a sample; kits for detecting a risk of cancer or presence of cancer in a patient; and vaccines comprising a BSNAs or BSP. The invention additionally discloses fragments, mutants, fusion proteins, homologous proteins and allelic variants of BSPs; methods for identifying and designing agonists' and antagonists of BSPs; methods for

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:21:14 ; Search time 56 Seconds  
(without alignments)  
1265.035 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSGLMSQEKVTSFYWEERI.....RLICDAYMCMQSFMSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgm2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	151	3.0	1427	4	US-09-538-092-1044
2	135	2.7	1043	4	US-09-949-016-11650
3	130.5	2.6	484	4	US-09-248-796A-24175
4	125.5	2.5	1469	4	US-09-262-537-58
5	118.5	2.4	1466	4	US-09-262-537-20
6	118.5	2.4	1471	4	US-08-811-519-1
7	118	2.3	267	3	US-09-399-913-57
8	118	2.3	267	4	US-09-350-614-57
9	118	2.3	677	4	US-09-270-767-45699
10	117	2.3	386	4	US-09-248-796A-17565
11	117	2.3	798	2	US-08-222-617A-8
12	115.5	2.3	719	4	US-09-949-016-7766
13	114	2.3	523	4	US-09-248-796A-17555
14	114	2.3	850	4	US-09-129-603-2
15	114	2.3	2777	4	US-10-220-587-4
16	113	2.2	1226	1	US-08-280-443-2
17	113	2.2	1226	1	US-08-457-459-2
18	113	2.2	1226	1	US-08-555-678-2
19	113	2.2	1226	5	PCT-US95-02275-2
20	112.5	2.2	493	3	US-08-999-774A-12
21	112.5	2.2	805	4	US-09-538-092-257
22	112	2.2	734	4	US-09-328-352-4412
23	112	2.2	869	4	US-09-902-540-10125
24	111.5	2.2	1317	4	US-09-949-016-7588
25	110.5	2.2	657	3	US-09-370-368-7
26	110	2.2	577	4	US-09-949-016-11572
27	109.5	2.2	868	4	US-09-538-092-787

28	109.5	2.2	1306	3	US-08-999-774A-13	Sequence 13, Appl
29	109	2.2	452	4	US-09-205-258-689	Sequence 689, App
30	109	2.2	667	4	US-09-949-016-7759	Sequence 7759, Ap
31	108.5	2.2	493	4	US-09-538-092-1210	Sequence 1210, Ap
32	108	2.1	533	4	US-08-216-592A-4	Sequence 4, Appl1
33	108	2.1	665	4	US-09-328-352-6983	Sequence 6983, Ap
34	108	2.1	753	4	US-09-949-016-6676	Sequence 6676, Ap
35	107.5	2.1	659	4	US-09-562-737-18	Sequence 18, Appl
36	107.5	2.1	897	4	US-09-538-092-315	Sequence 315, App
37	107.5	2.1	1477	4	US-09-206-942-71	Sequence 71, Appl
38	107.5	2.1	2616	6	5206163-3	Patent No. 5206163
39	107.5	2.1	2616	6	5206163-3	Patent No. 5206163
40	107	2.1	501	4	US-09-540-211A-1027	Sequence 1027, Ap
41	106.5	2.1	696	3	US-07-757-342D-4	Sequence 4, Appl1
42	106.5	2.1	696	4	US-09-461-657B-4	Sequence 4, Appl1
43	106.5	2.1	806	4	US-09-949-016-7572	Sequence 7572, Ap
44	106.5	2.1	1049	4	US-09-248-796A-18611	Sequence 18611, A
45	105.5	2.1	491	4	US-09-302-626B-191	Sequence 191, App

#### ALIGNMENTS

RESULT: 1  
US-09-538-092-1044  
Sequence 1044, Application #/09-538-092-1044  
Patent No. 675681A  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: Polypeptide Compositions and Methods of Use  
FIELD OF INVENTION: Polypeptide Compositions and Methods of Use  
CROSS REFERENCE TO RELATED APPLICATIONS: US/09-538-092-1044  
CURRENT APPLICATION NUMBER: 09-538-092-1044  
CURRENT FILING DATE: 2000-08-29  
PRIORITY APPLICATION NUMBER: 09/127,952  
PRIORITY FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuraPatSeqFormatter Version 0.9  
SEQ ID NO 1044  
LENGTH: 1427  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (0)-(0)  
OTHER INFORMATION: Polypeptide Accession Number P30622  
US-09-538-092-1044

Query Match						3*0%; Score 151; DB 4; Length 1427;
Best Local Similarity						20.5%; Pred. No. 0.00026;
Matches						99; Conservative 55; Mismatches 171; Indels 157; Gaps 20;
QY	260	GYFVGVDMPNPGNDGDFGVLCSQACVSTILLHINDIIPESVTQERRPPKLAEMSRG	319			
DB	85	GWAGIVLDEPKNDGVSAGVR-YFQCEP-----LKGIF-----TRPSKL-----TRK	127			
QY	320	VGDGSSSHNPKATGSTDGPNRSELYTLNGSSVDSPQSKNKTWYIDEVAEDPAK	379			
DB	128	V-----QAEDEANGLQTPASRATSPCTSTAGVSSSPSTFNS-----IPQPSQPA-	175			
QY	380	SLTEISTDFDRSPPLQPPPVNSLTTFENRFLSLTRKMPNTNGSIHSPLSLSAQSVN	439			
DB	176	-----AKPSATPISNLT-----KTASESIS	197			
QY	440	ELNTPAVQESPPPLAMPNGNSHGLEVGSAAEVKENPFYGVIRWIGOPGLNEVLAGELE	499			
DB	198	NLSEAGSIKK-----GERELKIGDRVLVGTKA--GVVRFLETDFAKGEMCGVEL	246			
QY	500	EDECACCTGTGTRGTYFTYFCALKKALFVKLKSCRPSRFLASLPVSNQIERCNSLAFGGY	559			
DB	247	-DEPLKNDGAVAGTRYFQCPKYGLFA-----PVHKVTKIGF----	283			

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:25:00 ; Search time 97 Seconds  
(without alignments)  
3251.750 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQEKVTSFYWEERI.....RLLCDAYMCWQSPMTSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubaa/PTCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubaa/PTCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	960	US-10-788-792-250	Sequence 250, App
2	4971.5	98.8	956	US-09-851-673-4	Sequence 4, Appli
3	4971.5	98.8	956	US-10-755-889-490	Sequence 490, App
4	3862	76.7	731	US-10-921-707-9	Sequence 9, Appli
5	1275	25.3	261	US-10-264-237-1609	Sequence 1609, Ap
6	1173	23.3	238	US-10-264-237-1610	Sequence 1610, Ap
7	597	11.9	113	US-09-864-761-34675	Sequence 34675, A
8	146	2.9	354	US-10-087-192-120	Sequence 120, App
9	143	2.8	547	US-10-108-260A-2751	Sequence 2751, Ap
10	143	2.8	547	US-10-275-595A-13	Sequence 13, Appli
11	135.5	2.7	306	US-10-104-047-2990	Sequence 2990, Ap
12	135.5	2.7	721	US-09-764-875-857	Sequence 857, App
13	135.5	2.7	2273	US-10-282-122A-66115	Sequence 66115, A

14	134.5	2.7	721	9	US-09-764-868-731	Sequence 731, App
15	134.5	2.7	721	11	US-09-764-875-1140	Sequence 1140, Ap
16	134.5	2.7	816	16	US-10-437-963-132799	Sequence 132799,
17	134	2.7	307	14	US-10-106-698-5606	Sequence 5606, Ap
18	133.5	2.7	1319	16	US-10-408-765A-343	Sequence 343, App
19	132.5	2.6	439	13	US-10-087-192-117	Sequence 117, App
20	130	2.6	717	15	US-10-369-493-22287	Sequence 22287, A
21	129.5	2.6	1281	16	US-10-363-829-373	Sequence 373, App
22	129.5	2.6	3298	14	US-10-160-758-16	Sequence 16, Appli
23	129.5	2.6	3298	14	US-10-174-677-8	Sequence 8, Appli
24	129.5	2.6	3298	15	US-10-120-801-51	Sequence 51, Appli
25	129.5	2.6	3298	15	US-10-210-172-50	Sequence 50, Appli
26	127.5	2.5	3217	15	US-10-311-623-8	Sequence 8, Appli
27	127	2.5	803	16	US-10-437-963-132702	Sequence 132702,
28	126.5	2.5	808	16	US-10-437-963-132681	Sequence 132681,
29	124	2.5	1474	14	US-10-225-567A-522	Sequence 522, App
30	124	2.5	1474	15	US-10-292-798-914	Sequence 914, App
31	124	2.5	2621	16	US-10-437-963-122168	Sequence 122168,
32	123.5	2.5	814	16	US-10-437-963-185098	Sequence 185098,
33	122.5	2.4	803	14	US-10-349-436-33	Sequence 33, Appli
34	122.5	2.4	892	15	US-10-276-774-1800	Sequence 1800, Ap
35	122.5	2.4	907	17	US-10-491-213-8	Sequence 8, Appli
36	122.5	2.4	1120	16	US-10-437-963-152821	Sequence 152821,
37	122.5	2.4	1282	16	US-10-437-963-110654	Sequence 110654,
38	122.5	2.4	1933	15	US-10-369-493-1945	Sequence 1945, Ap
39	121	2.4	2263	16	US-10-408-765A-2231	Sequence 2231, Ap
40	121	2.4	995	16	US-10-437-963-105117	Sequence 105117,
41	120.5	2.4	867	15	US-10-282-122A-57767	Sequence 57767, A
42	120.5	2.4	1033	9	US-09-888-615-75	Sequence 75, Appli
43	120.5	2.4	1109	15	US-10-425-114-72939	Sequence 72939, A
44	120.5	2.4	1471	10	US-09-998-027-4	Sequence 4, Appli
45	120.5	2.4	1471	14	US-10-165-099-4	Sequence 4, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-788-792-250  
; Sequence 250, Application US/10788792  
; Publication No. US20040191819A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Pharmaceuticals Corporation  
; APPLICANT: Eveleigh, Deepa  
; APPLICANT: Bigwood, Douglas  
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE  
; FILE REFERENCE: 5152  
; CURRENT APPLICATION NUMBER: US/10/788,792  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/450,655  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 250  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-788-792-250

Query Match	99.0%	Score	4983	DB	16	Length	960
Best Local Similarity	99.5%	Pred. No.	0				
Matches	948	Conservative	0	Mismatches	1	Indels	4
Gaps	4						
Qy	1	MSSGLWSQEKVTSFYWEERI	1	1	MSSGLWSQEKVTSFYWEERI	1	1
Db	8	MSSGLWSQEKVTSFYWEERI	8	8	MSSGLWSQEKVTSFYWEERI	8	8
Qy	61	PSAKKKNQIGLKILEQPHAVLFVDE-DVVEINEKFTLELLAITNCEERFSLFKNRRLS	61	61	PSAKKKNQIGLKILEQPHAVLFVDE-DVVEINEKFTLELLAITNCEERFSLFKNRRLS	61	61
Db	68	PSAKKKNQIGLKILEQPHAVLFVDEKDVVEINEKFTLELLAITNCEERFSLFKNRRLS	68	68	PSAKKKNQIGLKILEQPHAVLFVDEKDVVEINEKFTLELLAITNCEERFSLFKNRRLS	68	68
Qy	120	KGLQIDVGCVPKVLQSGEBKFPGVVRFPROPLAERTVSGIFPGVELLEGGCGFTDGV	120	120	KGLQIDVGCVPKVLQSGEBKFPGVVRFPROPLAERTVSGIFPGVELLEGGCGFTDGV	120	120

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 18, 2005, 15:26:40 ; Search time 8972 Seconds  
(without alignments)  
5125.279 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLNSQKVTSPYWEERI.....RLLCDAYMCYQSFMSLYK 949

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Qs/cgn2\_1/USPTO.spool\_p/US09671687/runat 18042005.115018.17125/app query.fasta\_1.1095  
-DB=GenEmbl -QFMT=fastap -SUFFIX=ige -MINMATCH=0.1 -LOOPT=0 -LOOPT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09671687 @CGN 1.1.5932 @runat 18042005.115018.17125 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Databases :

GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	3302	6	CQ834224
2	4983	99.0	3540	9	BC012342
3	4983	99.0	5414	9	AB020656
4	4980	98.9	3302	6	CQ834222

5	4971.5	98.8	5371	9	HS3450014
6	4968.5	98.7	3311	6	CQ834226
7	4962	98.6	3480	6	CQ719792
8	4942	98.2	4527	6	BD231207
9	4718.5	93.7	4314	10	AK122389
10	4718.5	93.7	4501	10	BC042438
11	4712	93.6	3287	10	BC082001
12	4601	91.4	2845	6	BD160617
13	4601	91.4	2845	6	AX883937
14	4601	91.4	2845	9	AK024348
15	4600.5	91.4	241990	2	AC123449
16	4600.5	91.4	251132	2	AC098162
17	3676	73.0	2523	6	AR338799
18	3433.5	68.2	2341	9	AK000187
19	3022.5	60.0	2569	6	BD160470
20	3022.5	60.0	2569	6	AX883681
21	3022.5	60.0	2569	9	AK024212
22	2930	58.2	1954	9	AK056226
23	2493	49.5	241630	2	AC11881
24	2468	49.0	2116	6	BD135433
25	2468	49.0	2116	6	CQ867781
26	2468	49.0	2116	6	AR534837
27	2108.5	41.9	182059	2	AX017216
28	2108.5	41.9	182059	2	AX13651
29	1736	34.5	251957	2	AC126867
30	1662	33.0	2426	10	BC049879
31	1442.5	28.7	212531	2	AC145178
32	1430.5	28.4	129025	2	AC145180
33	1370	27.2	1069	5	BX933038
34	1344	26.7	1335	5	EX934133
35	1262	25.1	837	6	BD149741
36	1262	25.1	837	6	AX869679
37	1215	24.1	758	6	BD147076
38	1215	24.1	758	6	AX867014
39	1132.5	22.5	2068	3	AY071592
40	1111	22.1	151567	2	AC145503
41	1111	22.1	199277	2	AC145445
42	1109.5	22.0	208061	2	AC145254
43	1108.5	22.0	168271	9	AC007728
44	1097.5	21.8	141663	2	AC145018
45	1095.5	21.8	163319	9	HS3403140

#### ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	CDS
CQ834224	CQ834224	Sequence 95 from Patent WO2004058805.	CQ834224	CQ834224.1	GI:50833761	Homo sapiens (human)	Homo sapiens	1	Matsuda, A. and Yoneta, S.	T cell activating gene	Patent: WO 2004058805-A 95 15-JUL-2004;	Asahi Kasei Pharma Corporation (JP)	Location/Qualifiers	
													1. .3302	
													/organism="Homo sapiens"	
													/mol_type="unassigned DNA"	
													/db_xref="taxon:9606"	
													243. .3104	
													/note="unnamed protein product"	
													/codon_start=1	
													/protein_id="CAH05327.1"	
													/db_xref="GI:50833762"	
													/translation="MSSGLNSQKVTSPYWEERI FYLLQECSTVDKQTKLKVPGK	
													SIGQVTDKRSVGHRSIPSAKGNQIGLKILBQPHAVLFDKSVVINEKPTTELLA	

linear PAT 29-JUL-2004

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 18, 2005, 15:25:35 ; Search time 1059 Seconds  
(without alignments)  
5304.848 Million cell updates/sec

Title: US-09-671-687A-3  
Perfect score: 5034  
Sequence: 1 MSSGLWQKVTSPYWERI.....RLLCDAYMCMQSPMTSLYK 949

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2 1/USPTO pool p/US0961687/runat 18042005 115017 17115/app query.fasta\_1.1095  
-DB=N Geneseq 16Dec04 -QMT=fastcap -SUFFIX=ring -MINMATCH=0 1 -LOOPCT=0  
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US0961687 @CGN 1 1 708 @runat 18042005 115017 17115 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04: \*  
1: Geneseqn1980s: \*  
2: Geneseqn1990s: \*  
3: Geneseqn2000s: \*  
4: Geneseqn2001as: \*  
5: Geneseqn2001bs: \*  
6: Geneseqn2002as: \*  
7: Geneseqn2002bs: \*  
8: Geneseqn2003as: \*  
9: Geneseqn2003bs: \*  
10: Geneseqn2003cs: \*  
11: Geneseqn2003ds: \*  
12: Geneseqn2004as: \*  
13: Geneseqn2004bs: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4983	99.0	3302	12 ADQ95917	Adq95917 T cell ac
2	4983	99.0	6831	10 ADC24898	Adc24898 Human bre
3	4980	98.9	3302	12 ADQ95915	Adq95915 T cell ac
4	4971.5	98.8	5371	10 ABV75394	Abv75394 Human CYL
5	4971.5	98.8	5371	13 ADRI4488	Adri4488 Human NF-

6	4968.5	98.7	3311	12 ADQ95919	Adq95919 T cell ac
7	4942	98.2	4527	3 AAA08589	Aaa08589 Human cyt
8	4601	91.4	2845	4 AAH18625	Aah18625 Human CDN
9	3876.5	77.0	4716	4 AAS41617	Aas41617 cDNA enco
10	3676	73.0	2523	4 AAI58410	Aai58410 Human pol
11	3676	73.0	2523	5 ADQ98620	Adq98620 DNA enco
12	3676	73.0	2523	9 ADB48380	Adb48380 Novel hum
13	3523	70.0	4286	4 AA160196	Aa160196 Human pol
14	3329	66.1	2488	4 AAS41081	Aas41081 cDNA enco
15	3022.5	60.0	2569	4 AAH18478	Aah18478 Human CDN
16	2468	49.0	2116	2 AAZ07515	Aaz07515 Human RAP
17	1778	35.3	1151	6 ABL89642	Ab189642 Human pol
18	1494	29.7	1013	6 ABL89643	Ab189643 Human pol
19	1490.5	29.6	1160	5 AAS90524	Aas90524 DNA enco
20	1262	25.1	758	4 AAH07749	Aah07749 Human CDN
21	1215	24.1	758	4 AAH05084	Aah05084 Human CDN
22	1102	21.9	617	6 ABQ60558	Abq60558 Human col
23	936	18.6	5433	4 ABL09704	Ab109704 Drosophil
24	879	17.5	557	6 ABQ60559	Abq60559 Human col
25	867.5	17.2	8990	4 AAK77783	Aak77783 Human imm
26	856	17.0	1655	4 ABL09705	Ab109705 Drosophil
27	626	12.4	376	8 ABX51704	Abx51704 Bovine ES
28	568	11.3	318	12 ADK71948	Adk71948 Human ori
29	545	10.8	303	12 ADK71946	Adk71946 Human ori
30	545	10.8	309	4 AAI20692	Aai20692 Probe #10
31	545	10.8	309	4 ABA65741	Ab65741 Human foe
32	545	10.8	309	4 AAI45907	Aai45907 Probe #14
33	545	10.8	309	4 ABA47848	Ab47848 Human bre
34	545	10.8	309	4 ABA32825	Ab32825 Probe #11
35	545	10.8	309	4 AAK39883	Aak39883 Human bon
36	545	10.8	309	4 AAK14143	Aak14143 Human bra
37	545	10.8	309	5 AAI06390	Aai06390 Probe #63
38	545	10.8	309	6 ABS13981	Ab13981 Human gen
39	514	10.2	288	12 ADK71950	Adk71950 Human ori
40	512	10.2	483	4 AAI11479	Aai11479 Probe #14
41	512	10.2	483	4 ABA53149	Ab53149 Human foe
42	512	10.2	483	4 AAI32754	Aai32754 Probe #14
43	512	10.2	483	4 ABA42721	Ab42721 Human bre
44	512	10.2	483	4 ABA22920	Ab22920 Probe #13
45	512	10.2	483	4 AAK36850	Aak36850 Human bon

ALIGNMENTS

RESULT 1  
ADQ95917  
ID ADQ95917 standard; CDNA; 3302 BP.  
XX  
AC ADQ95917;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE T cell activation associated CDNA #48.  
XX

ss; gene; anti-allergic; antiarthritic; antidiabetic;  
anti-HIV; antimicrobial; antirheumatic; immunosuppressive;  
neuroprotective; gene therapy; T cell activation; diagnosis;  
autoimmune disease; rheumatoid arthritis; asthma; multiple sclerosis;  
diabetes; allergic disease; infectious disease; AIDS; chronic rejection;  
organ; bone-marrow transplant.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT CDS 243..3104  
FT /\*tag= a  
XX  
XX WC2004058805-A2.  
XX  
XX 15-JUL-2004.  
XX  
XX 25-DEC-2003; 2003WO-JP016715.  
XX

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 18, 2005, 15:33:50 ; Search time 376 Seconds  
(without alignments)  
4129.858 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQKVTSPYWEIRI.....RLLCDAYMCMYQSTMSLYK 949

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US09671687/runat 18042005 115019 17155/app\_query.fasta\_1.1095  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORES=ptct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09671687@cgn1 1 105 @runat 18042005 115019 17155 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3676	73.0	2523	4	US-09-620-312D-290
2	2468	49.0	2116	4	US-09-646-403-3
3	185	3.7	110	4	US-09-513-999C-20085
4	151	3.0	5857	4	US-09-220-132-79
5	139	2.8	2825	4	US-09-949-016-1895
6	139	2.8	3130	4	US-09-949-016-5779
7	135	2.7	2643	3	US-09-399-913-56
8	135	2.7	2643	4	US-09-350-614-56
9	133	2.6	3245	4	US-09-774-528-352
10	130.5	2.6	1452	4	US-09-248-796A-10072
11	128.5	2.6	5610	4	US-09-262-537-57
12	126	2.5	1503	3	US-08-999-774A-11

13	126	2.5	4282	4	US-09-976-594-799	Sequence 799, App
14	126	2.5	4674	4	US-09-949-016-1717	Sequence 1717, Ap
15	122.5	2.4	1463	4	US-09-270-767-15085	Sequence 15085, A
c 16	122.5	2.4	31826	4	US-09-902-540-1256	Sequence 1256, Ap
c 17	121.5	2.4	13977	3	US-09-484-9708-60	Sequence 60, Appl
c 18	121.5	2.4	24333	4	US-09-639-207-9	Sequence 9, Appli
19	119.5	2.4	3545	3	US-08-885-291-54	Sequence 54, Appl
20	119.5	2.4	3545	3	US-09-496-672-54	Sequence 54, Appl
21	119.5	2.4	5715	3	US-09-107-847-1	Sequence 1, Appli
22	119	2.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
23	118.5	2.4	5391	4	US-08-811-519-2	Sequence 2, Appli
24	118.5	2.4	5693	4	US-09-262-537-19	Sequence 19, Appl
25	118	2.3	1380	3	US-09-239-303-1	Sequence 1, Appli
26	118	2.3	2033	4	US-09-270-767-14130	Sequence 14130, A
c 27	118	2.3	2418	4	US-09-614-221A-495	Sequence 495, App
c 28	118	2.3	16047	4	US-09-902-540-1136	Sequence 1136, Ap
29	118	2.3	36820	4	US-09-949-016-16665	Sequence 16665, A
30	117.5	2.3	1794	4	US-09-949-016-2105	Sequence 2105, Ap
31	117.5	2.3	4926	2	US-08-853-310-1	Sequence 1, Appli
32	117	2.3	1158	4	US-09-248-796A-3462	Sequence 3462, Ap
33	117	2.3	2729	1	US-08-412-431-2	Sequence 2, Appli
34	117	2.3	2729	3	US-08-623-679-2	Sequence 2, Appli
35	117	2.3	2729	3	US-08-933-774-2	Sequence 2, Appli
36	117	2.3	2729	3	US-09-181-030-2	Sequence 2, Appli
37	117	2.3	2729	3	US-09-534-242-2	Sequence 2, Appli
38	117	2.3	2729	3	US-09-454-854-2	Sequence 2, Appli
39	117	2.3	2729	3	US-09-164-671-2	Sequence 2, Appli
40	117	2.3	2729	4	US-09-182-113-2	Sequence 2, Appli
41	117	2.3	2729	4	US-08-862-442-2	Sequence 2, Appli
c 42	116.5	2.3	1869	4	US-09-489-039A-3406	Sequence 3406, Ap
43	115.5	2.3	6671	1	US-08-280-443-1	Sequence 1, Appli
44	115.5	2.3	6671	1	US-08-457-459-1	Sequence 1, Appli
45	115.5	2.3	6671	1	US-08-555-678-1	Sequence 1, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-620-312D-290  
; Sequence 290, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyang  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yungling  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 290  
; LENGTH: 2523  
; TYPE: DNA



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 18, 2005, 18:28:51 ; Search time 1146 Seconds  
(without alignments)  
5023.830 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSEKVTSPYWEERI.....RLLCDAYMCVMQSPMSLYK 949

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5522541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPTO.spool.p/US09671687/runat\_18042005\_115020\_17247/app.query.fasta\_1.1095  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blseqsum2  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09671687@cgn\_1.1.723 @runat\_18042005\_115020\_17247  
-NCFU=6 -ICFU=3 -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:\*\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/PCTUS\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4971.5	98.8	5371	10	US-09-851-673-3	Sequence 3
2	4971.5	98.8	5371	18	US-10-755-889-489	Sequence 489
3	4942	98.2	4527	18	US-10-921-707-25	Sequence 25
4	3676	73.0	2523	15	US-10-037-270-290	Sequence 290
5	3676	73.0	2523	17	US-10-117-722-290	Sequence 290
6	2468	49.0	2116	18	US-10-761-370-3	Sequence 3
C 7	1778	35.3	1151	17	US-10-264-237-204	Sequence 204
8	1494	29.7	1013	17	US-10-264-237-205	Sequence 205
C 9	1102	21.9	617	11	US-09-969-034-4253	Sequence 4253
C 10	879	17.5	557	11	US-09-969-034-4254	Sequence 4254
11	626	12.4	376	9	US-09-983-965-1633	Sequence 1633
C 12	545	10.8	309	9	US-09-864-761-18145	Sequence 18145
C 13	512	10.2	483	9	US-09-864-761-1386	Sequence 1386
14	412	8.2	425	10	US-09-918-995-35878	Sequence 35878
15	160.5	3.2	4847	17	US-10-152-319A-1764	Sequence 1764
16	151	3.0	5857	10	US-09-873-367C-305	Sequence 305
17	151	3.0	5857	19	US-10-843-641A-305	Sequence 305
18	148	2.9	3051	17	US-10-371-905A-3	Sequence 3
19	146	2.9	1380	13	US-10-087-192-119	Sequence 119
20	146	2.9	5563	18	US-10-723-860-1545	Sequence 1545
21	146	2.9	5607	18	US-10-723-860-5973	Sequence 5973
22	143	2.8	3287	17	US-10-275-595A-47	Sequence 47
23	143	2.8	3370	17	US-10-108-260A-308	Sequence 308
24	143	2.8	3592	10	US-09-814-353-20078	Sequence 20078
25	138	2.7	2154	17	US-10-369-493-45974	Sequence 45974
26	138	2.7	2451	18	US-10-437-963-30316	Sequence 30316
C 27	136.5	2.7	3409	18	US-10-723-860-6186	Sequence 6186
28	135.5	2.7	2618	17	US-10-104-047-1020	Sequence 1020
29	135.5	2.7	3103	11	US-09-764-875-259	Sequence 259
30	135.5	2.7	6822	17	US-10-282-122A-29931	Sequence 29931
31	135	2.7	2643	9	US-09-350-874-56	Sequence 56
32	135	2.7	2643	15	US-10-106-989-56	Sequence 56
33	134.5	2.7	3103	9	US-09-764-868-118	Sequence 118
34	134.5	2.7	3103	11	US-09-764-875-542	Sequence 542
35	134	2.7	1099	15	US-10-106-698-1329	Sequence 1329
36	134	2.7	2855	17	US-10-094-749-919	Sequence 919
37	133	2.6	3245	17	US-10-120-988-352	Sequence 352
38	132.5	2.6	1416	13	US-10-087-192-116	Sequence 116
39	132	2.6	3338	19	US-10-491-213-65	Sequence 65
40	130	2.6	2676	17	US-10-276-774-450	Sequence 450
41	129.5	2.6	4839	18	US-10-363-829-121	Sequence 121
42	129.5	2.6	10531	14	US-10-160-758-10	Sequence 10
43	129.5	2.6	10759	17	US-10-210-172-49	Sequence 49
44	128.5	2.6	2446	9	US-09-801-275-1	Sequence 1
45	128.5	2.6	2446	16	US-10-170-789-58	Sequence 58

#### ALIGNMENTS

#### RESULT 1

US-09-851-673-3  
; Sequence 3, Application US/09851673  
; Publication No. US20030165985A1  
; GENERAL INFORMATION:  
; APPLICANT: Derry, Jonathan  
; APPLICANT: Fanslow, William  
; APPLICANT: Dougall, William  
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING  
; FILE REFERENCE: 3198  
; CURRENT APPLICATION NUMBER: US/09/851,673  
; CURRENT FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 5371  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:18:59 ; Search time 22 Seconds  
(without alignments)  
4150.441 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSGSLWSQEKVTSYWEERI.....RLLCDAYMCVQSPMSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	613.5	12.2	1021	2 F88568	protein F40F12.5 [
2	590.5	11.7	727	2 S42334	F40F12.5 protein -
3	151	3.0	1352	2 A43336	microtubule-vesicl
4	151	3.0	1427	2 S22595	restin - human
5	149.5	3.0	1046	2 T42734	cytoplasmic linker
6	149	3.0	1046	2 T42720	cytoplasmic linker
7	135.5	2.7	2273	2 T09083	hemagglutinin/hemo
8	130	2.6	717	2 S38177	SSV7 protein homol
9	125.5	2.5	1921	2 T13827	kinesin-73 - fruit
10	124.5	2.5	1146	2 F83853	5-methyltetrahydro
11	124	2.5	3624	2 AD0835	large repetitive p
12	122.5	2.4	1953	2 S63244	BNI1 protein - yea
13	122	2.4	1791	2 T02345	hypothetical prote
14	121	2.4	1498	2 E86302	hypothetical prote
15	121	2.4	1641	2 T10955	early nodulin bind
16	120	2.4	499	2 S56265	hypothetical prote
17	119	2.4	662	2 T18233	probable transcrip
18	118.5	2.4	1466	2 T17138	CluA protein - ra
19	118.5	2.4	1467	2 T18411	latrophilin-1, bra
20	118.5	2.4	1471	2 T17149	CluA protein - ra
21	118.5	2.4	1472	2 T18413	latrophilin-1, bra
22	118.5	2.4	1510	2 T17145	CluA protein - ra
23	118.5	2.4	1515	2 T17156	CluBB protein - ra
24	116.5	2.3	825	2 T47164	hypothetical prote
25	116.5	2.3	2484	2 T26216	hypothetical prote
26	116.5	2.3	2607	2 T26215	hypothetical prote
27	115.5	2.3	514	2 T25509	hypothetical prote
28	115.5	2.3	670	2 T38446	microtubule-associ
29	115.5	2.3	673	2 S35335	transcription fact

30	115.5	2.3	1341	2 T17285	hypothetical prote
31	115	2.3	471	2 S57591	hypothetical prote
32	114.5	2.3	752	2 D96699	hypothetical prote
33	114.5	2.3	1161	2 B70387	DNA polymerase III
34	114.5	2.3	1357	2 S61187	probable membrane
35	114	2.3	438	2 T39772	ubiquitin carboxyl
36	114	2.3	739	2 T15215	hypothetical prote
37	113.5	2.3	974	2 D89057	protein K09H1.1 [
38	113.5	2.3	1335	2 T18289	racGAP protein - s
39	113.5	2.3	2700	2 D88450	protein F21H11.2 [
40	113	2.2	753	2 A96747	probable RNA-bindi
41	113	2.2	1226	1 S65593	adenosine deaminas
42	112.5	2.2	642	2 T10861	phascolin G-box bi
43	112.5	2.2	805	2 S50277	ubiquitin-specific
44	112.5	2.2	1116	2 T54378	gene X104 protein
45	112	2.2	3685	1 A27605	dystrophin, muscle

ALIGNMENTS

RESULT 1

F88568

Protein F40F12.5 [imported] - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C/Accession: F88568

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A/Reference number: A75000; PMID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects/C.el

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A/Accession: F88568

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1021 <STO>

A/Cross-references: GB:chr\_III; PIDN:CAA82939.1; PID:g3877002; GSPDB:GN00021; CESP:F40F

C/Genetics:

A/Gene: F40F12.5

A/Map position: 3

Query Match	12.2%	Score	613.5	DB 2	Length	1021			
Best Local Similarity	23.7%	Pred. No.	4.6e-34						
Matches	256	Conservative	154	Mismatches	315	Indels	357	Gaps	46
QY	103	TNCEERFSLP	-----KNRRLSKGLQIDVCGCPVKQLRSGBEKKPGVVFRFGPLLAERTV	157					
Db	43	TQSEKSNLYTSENTSNRLNLNQNPVGT	-----	73					
QY	158	SGIFFGVLEEGRCOGFTDGVYQKQLFCQDEDCGFVALDKLELIEDDDTALE	-----	211					
Db	74	--LIDGFELINEASGSGFLD	-----DQL	-----VDVSDYSRDRTTKLDNRNSP	115				
QY	212	-----SDYAGPGDTQWVELPPLLEI	-----	NSRVS	235				
Db	116	ELIVALQLQKVGIRFSNNYGRREEPCVHIPTGVREMAADDDKMSLKEWFTKSRAS	175						
QY	236	--LKGG-----ETIESGTWIFC	-----DVLPGKESLGYFVGVDMDNPTGNWDGRFDGV	281					
Db	176	SHLRDGLAMPMBELDC--TPLICAMITRSDVMRNQQAIIHLAVSVEKRI	-----	EV	226				
QY	282	LCSFACVESTILLHINDIIPESV--TQERRPPKLAFNMRGCVGDKG	-----	324					
Db	227	YQNFEWFNFILNLKIGDSVSEVDETMRRYPAKVSWIGERPEASGIWYVNDPQNTSQWP	286						
QY	325	-----SSGHNKP-----KATGSTS--DPCNRRSELYFTLN	-----	GSSVDS--	358				
Db	287	SSNQSYSSSHDLRLNRQFDTNWFEMSGSSSVAFSN--SRLYYSPNQMHMPKGGGVVALY	344						
QY	359	-----QPQSKSKNTWYIDEVADPPAKSLTEIS	385						
Db	345	DNRLRQVSGDEQYRSAPKAPRERIIPVSRQOPETEQRN	-----SRSMKPSE	393					

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 18, 2005, 15:32:50 ; Search time 6177 Seconds  
(without alignments)  
5847.983 Million cell updates/sec

Title: US-09-671-687A-3  
Perfect score: 5034  
Sequence: 1 MSSGLWQKVTSPYWEERI.....RLLCDAYMCYQSPMSLYK 949

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-Q/cgn2 1/USPTO spool p/US09671687/runat 18042005 115018 17139/app\_query.fasta\_1.1095  
-DB=EST -OPMT=fastcap -SUPPIX=rat -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09671687 @CGN 1 1 5180 @runat 18042005 115018 17139 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gest1.\*  
9: gb\_gest2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4494	89.3	3496	3 AF161542	Homo sapi
2	4313	85.7	2862	9 AY406374	Homo sapi
3	4102	81.5	2730	9 AY406376	Mus muscu
4	3768	74.9	2862	9 AY406375	Pan trogl
5	2952	58.6	2220	3 AK039054	Mus muscu
6	2769	55.0	3137	3 BC028885	Mus muscu
7	1572.5	31.2	1063	5 BQ433523	AGENCOURT
8	1570	31.2	1039	4 BM457960	AGENCOURT
9	1459.5	29.0	1478	3 AK042764	Mus muscu

10	1435	28.5	938	4 BI666276	BI666276
11	1426	28.3	2218	3 AK048183	Mus muscu
12	1416.5	28.1	1133	4 BM480127	AGENCOURT
13	1384	27.5	812	6 CA512526	UI-R-FJO-
14	1363	27.1	1892	3 BC024596	Mus muscu
15	1340	26.6	837	4 BG867631	602787414
16	1302	25.9	816	5 BQ442079	UI-M-EXO-
17	1288	25.6	721	5 BP162259	BP162259
18	1286.5	25.6	889	5 BU505487	AGENCOURT
19	1280	25.4	783	4 BM016881	603643383
20	1268.5	25.2	715	7 CN157036	944487 MA
21	1267.5	25.2	840	5 BP144628	BP144628
22	1262	25.1	837	1 AU137267	AU137267
23	1235	24.5	726	7 CR772310	DKFZp468L
24	1233	24.5	717	7 CF750356	UI-M-HJO-
25	1215	24.1	758	1 AU122742	AU122742
26	1202.5	23.9	791	7 CN461343	UI-M-HNO-
27	1198	23.8	743	6 CD351332	UI-M-GIO-
28	1170	23.2	677	6 CD626856	56076837J
29	1165	23.1	648	1 AL707441	DKFZp686M
30	1160.5	23.1	697	4 BM724143	UI-E-EOI-
31	1158	23.0	781	7 CK636353	UI-M-HNO-
32	1152	22.9	826	7 CK597829	AGENCOURT
33	1151	22.9	708	6 CB466941	732655 MA
34	1152	22.9	794	2 BF141863	601791346
35	1139.5	22.6	770	4 BI906770	603064511
36	1139.5	22.6	785	6 CB235676	AGENCOURT
37	1128	22.4	906	5 BU461394	603774393
38	1127.5	22.4	907	5 BQ438227	AGENCOURT
39	1118	22.2	702	2 BB648023	BB648023
40	1117.5	22.2	755	7 CO404877	AGENCOURT
41	1107.5	22.0	723	6 CD559213	AGENCOURT
42	1105.5	22.0	1134	5 BM904688	AGENCOURT
43	1102	21.9	637	2 AW985722	AW985722
44	1094	21.7	639	7 CN704295	E0485H10-
45	1092.5	21.7	1365	3 AY383658	Rattus no

#### ALIGNMENTS

RESULT 1  
AF161542 LOCUS AF161542 3496 bp mRNA linear HTC 22-MAY-2001  
DEFINITION Homo sapiens HSPC057 mRNA, complete cds.  
ACCESSION AF161542  
VERSION AF161542.1 GI:6841351  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3496)  
Zhang, Q.H., Ye, M., Wu, X.Y., Ren, S.X., Zhao, M., Zhao, C.J., Fu, G., Shen, Y., Fan, H.Y., Lu, G., Zhong, M., Xu, X.R., Han, Z.G., Zhang, J.W., Tao, J., Huang, Q.H., Zhou, J., Hu, G.X., Gu, J., Chen, S.J. and Chen, Z. Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells  
JOURNAL Genome Res. 10 (10), 1546-1560 (2000)  
MEDLINE 20499367  
PUBMED 11042152  
REFERENCE 2 (bases 1 to 3496)  
Zhang, Q.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L., Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z. Human full length cDNA cloned from cd34+ stem cells  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 3496)  
Zhang, Q.H., Ye, M., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L., Fan, H.Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z. Direct Submission  
JOURNAL Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:16:44 ; Search time 65 Seconds  
(without alignments)  
7476.356 Million cell updates/sec

Title: US-09-671-687A-3

Perfect score: 5034

Sequence: 1 MSSGLWSQEKVTSFYWEERI.....RLLCDAYMCMYQSPMSLYK 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4971.5	98.8	956	1	CYLD HUMAN
2	4718.5	93.7	952	1	CYLD_MOUSE
3	4712	93.6	953	2	Q66H62
4	4207	24.0	778	2	Q7Q414
5	1136.5	22.6	551	2	O8IPC3
6	1136.5	22.6	551	2	O8IPC5
7	1134	22.5	550	2	O8IPC4
8	1132.5	22.5	639	2	Q8SYF0
9	1092.5	21.7	454	2	Q6TXJ6
10	856	17.0	517	2	Q9VL04
11	619	12.3	1144	2	Q7JMS4
12	183.5	3.6	258	2	Q7PJA3
13	153.5	3.0	528	2	Q6BU87
14	151	3.0	653	2	Q6PS29
15	149.5	3.0	1046	2	O55156
16	149.5	3.0	1046	2	O55156
17	149	3.0	1046	2	Q9Z0H8
18	147.5	2.9	449	2	Q86WU4
19	146	2.9	350	2	Q6PTA3
20	145	2.9	547	2	Q96D25
21	145	2.9	1556	2	Q9VVRP1
22	143.5	2.9	495	2	Q6FM69
23	143.5	2.9	1047	2	Q9EP81
24	143	2.8	547	2	Q8WU11
25	142.5	2.8	1606	2	Q7PV08
26	142	2.8	1012	2	Q7TS19
27	141	2.8	1012	2	Q8CHU1
28	141	2.8	1429	2	Q6DFE6
29	140.5	2.8	429	2	Q96C99
30	140	2.8	924	2	Q7VDY2
31	139.5	2.8	1921	2	Q86BR0

#### ALIGNMENTS

##### RESULT 1

ID	CYLD HUMAN	STANDARD;	PRT;	956 AA.
AC	Q9NCQ7; Q94934; Q7L3N6; Q96EH0; Q9NZX9;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Probable ubiquitin carboxyl-terminal hydrolase CYLD (EC 3.1.2.15)			
DE	(Ubiquitin thiolesterase CYLD) (Ubiquitin-specific processing protease CYLD) (Deubiquitinating enzyme CYLD) (HSPC057).			
GN	Name=CYLD; Synonyms=CYLD1, KIAA0849;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RI	[1]			
RN	SEQUENCE FROM N.A. (ISOFORM 1), DISEASE, AND TISSUE SPECIFICITY.			
RX	MEDLINE=20296617; PubMed=10835629; DOI=10.1038/76006;			
RA	Bignell G.R., Brown C., Biggs P.J., Lakhani S.R., Jones C., Hansen J., Blair E., Hofmann B., Siebert R., Turner G., Evans D.G., Schrander-Stumpel C., Beemer F.A., Van Den Ouweland A., Halley D., Delpech B., Cleveland M.G., Leigh I., Leisti J., Rasmussen S., Wallace M.R., Fenske C., Banerjee P., Oiso N., Chaggar R., Merrett S., Leonard N., Huber M., Hohl D., Chapman P., Burn J., Swift S., Smith A., Ashworth A., Stratton M.R.;			
RT	"Identification of the familial cylindromatosis tumor suppressor gene.";			
RL	Nat. Genet. 25:160-165 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Brain;			
RX	MEDLINE=99156230; PubMed=10048485;			
RA	Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";			
RL	DNA Res. 5:355-364 (1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Uterus;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			

32	139	2.8	446	2	Q757P1
33	138.5	2.8	1172	2	Q7RF04
34	138.5	2.8	1937	2	Q6A062
35	138	2.7	724	2	Q8BWD1
36	138	2.7	1024	2	O14527
37	138	2.7	1391	2	Q922J3
38	137.5	2.7	992	2	Q6C1K8
39	137	2.7	868	2	Q9SDN6
40	136.5	2.7	359	2	Q7PV06
41	136	2.7	887	2	Q6FQF0
42	135.5	2.7	2273	2	O31152
43	135.5	2.7	2273	2	Q7DD88
44	135	2.7	1046	2	Q9UDT6
45	134.5	2.7	657	2	Q7Z3N8

Q757P1	ashbya goss
Q7RF04	plasmidium
Q6A062	mus musculus
Q8BWD1	mus musculus
O14527	homo sapien
Q922J3	mus musculus
Q6C1K8	yarrowia li
Q9SDN6	nicotiana t
Q7PV06	anopheles g
Q6FQF0	candida gla
O31152	neisseria m
Q7DD88	neisseria m
Q9UDT6	homo sapien
Q7Z3N8	homo sapien